RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/047,253 A

Source: IFWJ6

Date Processed by STIC: 6/19/06

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RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: **US/10/047,253A**   TIME: 10:18:13

Input Set : **A:\CIT1510-4.ST25.txt**
Output Set: **N:\CRF4\06142006\J047253A.raw**

```
 3 <110> APPLICANT: CALIFORNIA INSTITUTE OF TECHNOLOGY
 4        COPE, Gregory
 5        VERMA, Rati
 6        ARAVIND, L.
 7        KOONIN, Eugene V.
 8        DESHAIES, Raymond
 9        AMBROGGIO, Xavier
11 <120> TITLE OF INVENTION: REGULATION OF TARGET PROTEIN ACTIVITY THROUGH MODIFIER
PROTEINS
13 <130> FILE REFERENCE: JHU1510-4
15 <140> CURRENT APPLICATION NUMBER: US 10/047,253A
16 <141> CURRENT FILING DATE: 2002-01-14
18 <150> PRIOR APPLICATION NUMBER: US 60/261,314
19 <151> PRIOR FILING DATE: 2001-01-12
21 <150> PRIOR APPLICATION NUMBER: US 60/322,322
22 <151> PRIOR FILING DATE: 2001-09-14
24 <150> PRIOR APPLICATION NUMBER: US 60/322,030
25 <151> PRIOR FILING DATE: 2001-09-14
27 <160> NUMBER OF SEQ ID NOS: 24
29 <170> SOFTWARE: PatentIn version 3.3
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 14
33 <212> TYPE: PRT
34 <213> ORGANISM: Artificial sequence
36 <220> FEATURE:
37 <223> OTHER INFORMATION: JAM domain
40 <220> FEATURE:
41 <221> NAME/KEY: MISC_FEATURE
42 <222> LOCATION: (1)..(14)
43 <223> OTHER INFORMATION: Xaa is any amino acid
45 <400> SEQUENCE: 1
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W--> 47 **His Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asp**
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52 <211> LENGTH: 17
53 <212> TYPE: PRT
54 <213> ORGANISM: Artificial sequence
56 <220> FEATURE:
57 <223> OTHER INFORMATION: JAM domain
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61 <221> NAME/KEY: MISC_FEATURE
62 <222> LOCATION: (3)..(3)
63 <223> OTHER INFORMATION: Xaa is Tyr or Ile
65 <220> FEATURE:
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 66 <221> NAME/KEY: MISC_FEATURE
 67 <222> LOCATION: (5)..(5)
 68 <223> OTHER INFORMATION: Xaa is Ser or Thr
 70 <220> FEATURE:
 71 <221> NAME/KEY: MISC_FEATURE
 72 <222> LOCATION: (8)..(16)
 73 <223> OTHER INFORMATION: Xaa is any amino acid
 75 <400> SEQUENCE: 2
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 81 Asp
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 86 <211> LENGTH: 246
 87 <212> TYPE: PRT
 88 <213> ORGANISM: Homo sapiens
 90 <400> SEQUENCE: 3
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 96 Thr Arg Val Asn Ala Gln Ala Ala Ala Tyr Glu Tyr Met Ala Ala Tyr
 97             20                  25                  30
100 Ile Glu Asn Ala Lys Gln Val Gly Arg Leu Glu Asn Ala Ile Gly Trp
101         35                  40                  45
104 Tyr His Ser His Pro Gly Tyr Gly Cys Trp Leu Ser Gly Ile Asp Val
105     50                  55                  60
108 Ser Thr Gln Met Leu Asn Gln Gln Phe Gln Glu Pro Phe Val Ala Val
109 65                  70                  75                  80
112 Val Ile Asp Pro Thr Arg Thr Ile Ser Ala Gly Lys Val Asn Leu Gly
113                 85                  90                  95
116 Ala Phe Arg Thr Tyr Pro Lys Gly Tyr Lys Pro Pro Asp Glu Gly Pro
117             100                 105                 110
120 Ser Glu Tyr Gln Thr Ile Pro Leu Asn Lys Ile Glu Asp Phe Gly Val
121             115                 120                 125
124 His Cys Lys Gln Tyr Tyr Ala Leu Glu Val Ser Tyr Phe Lys Ser Ser
125     130                 135                 140
128 Leu Asp Arg Lys Leu Leu Glu Leu Leu Trp Asn Lys Tyr Trp Val Asn
129 145                 150                 155                 160
132 Thr Leu Ser Ser Ser Ser Leu Leu Thr Asn Ala Asp Tyr Thr Thr Gly
133                 165                 170                 175
136 Gln Val Phe Asp Leu Ser Glu Lys Leu Glu Gln Ser Glu Ala Gln Leu
137             180                 185                 190
140 Gly Arg Gly Ser Phe Met Leu Gly Leu Glu Thr His Asp Arg Lys Ser
141         195                 200                 205
144 Glu Asp Lys Leu Ala Lys Ala Thr Arg Asp Ser Cys Lys Thr Thr Ile
145     210                 215                 220
148 Glu Ala Ile His Gly Leu Met Ser Gln Val Ile Lys Asp Lys Leu Phe
149 225                 230                 235                 240
152 Asn Gln Ile Asn Ile Ser
153                 245
156 <210> SEQ ID NO: 4
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        Input Set : A:\CIT1510-4.ST25.txt
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157 <211> LENGTH: 245
158 <212> TYPE: PRT
159 <213> ORGANISM: Homo sapiens
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167 Val Ser Val Glu Ala Val Asp Pro Val Phe Gln Ala Lys Met Leu Asp
168   20   25   30
171 Met Leu Lys Gln Thr Gly Arg Pro Glu Met Val Val Gly Trp Tyr His
172   35   40   45
175 Ser His Pro Gly Phe Gly Cys Trp Leu Ser Gly Val Asp Ile Asn Thr
176   50   55   60
179 Gln Gln Ser Phe Glu Ala Leu Ser Glu Arg Ala Val Ala Val Val Val
180 65   70   75   80
183 Asp Pro Ile Gln Ser Val Lys Gly Lys Val Val Ile Asp Ala Phe Arg
184   85   90   95
187 Leu Ile Asn Ala Asn Met Met Val Leu Gly His Glu Pro Arg Gln Thr
188   100   105   110
191 Thr Ser Asn Leu Gly His Leu Asn Lys Pro Ser Ile Gln Ala Leu Ile
192   115   120   125
195 His Gly Leu Asn Arg His Tyr Tyr Ser Ile Thr Ile Asn Tyr Arg Lys
196   130   135   140
199 Asn Glu Leu Glu Gln Lys Met Leu Leu Asn Leu His Lys Lys Ser Trp
200 145   150   155   160
203 Met Glu Gly Leu Thr Leu Gln Asp Tyr Ser Glu His Cys Lys His Asn
204   165   170   175
207 Glu Ser Val Val Lys Glu Met Leu Glu Leu Ala Lys Asn Tyr Asn Lys
208   180   185   190
211 Ala Val Glu Glu Glu Asp Lys Met Thr Pro Glu Gln Leu Ala Ile Lys
212   195   200   205
215 Asn Val Gly Lys Gln Asp Pro Lys Arg His Leu Glu Glu His Val Asp
216   210   215   220
219 Val Leu Met Thr Ser Asn Ile Val Gln Cys Leu Ala Ala Met Leu Asp
220 225   230   235   240
223 Thr Val Val Phe Lys
224   245
227 <210> SEQ ID NO: 5
228 <211> LENGTH: 421
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <400> SEQUENCE: 5
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238 Ala Leu Ser Lys Leu Gly Cys Asn Ile Thr Ile Ser Glu Asp Ile Thr
239   20   25   30
242 Pro Arg Arg Tyr Phe Arg Ser Gly Val Glu Met Glu Arg Met Ala Ser
243   35   40   45
246 Val Tyr Leu Glu Glu Gly Asn Leu Glu Asn Ala Phe Val Leu Tyr Asn
247   50   55   60

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250 Lys Phe Ile Thr Leu Phe Val Glu Lys Leu Pro Asn His Arg Asp Tyr
251 65                  70              75                  80
254 Gln Gln Cys Ala Val Pro Glu Lys Gln Asp Ile Met Lys Lys Leu Lys
255              85              90                  95
258 Glu Ile Ala Phe Pro Arg Thr Asp Glu Leu Lys Asn Asp Leu Leu Lys
259         100             105                 110
262 Lys Tyr Asn Val Glu Tyr Gln Glu Tyr Leu Gln Ser Lys Asn Lys Tyr
263         115             120                 125
266 Lys Ala Glu Ile Leu Lys Lys Leu Glu His Gln Arg Leu Ile Glu Ala
267     130             135                 140
270 Glu Arg Lys Arg Ile Ala Gln Met Arg Gln Gln Gln Leu Glu Ser Glu
271 145             150             155                 160
274 Gln Phe Leu Phe Phe Glu Asp Gln Leu Lys Lys Gln Glu Leu Ala Arg
275              165             170                 175
278 Gly Gln Met Arg Ser Gln Gln Thr Ser Gly Leu Ser Glu Gln Ile Asp
279         180             185                 190
282 Gly Ser Ala Leu Ser Cys Phe Ser Thr His Gln Asn Asn Ser Leu Leu
283         195             200                 205
286 Asn Val Phe Ala Asp Gln Pro Asn Lys Ser Asp Ala Thr Asn Tyr Ala
287     210             215                 220
290 Ser His Ser Pro Pro Val Asn Arg Ala Leu Thr Pro Ala Ala Thr Leu
291 225             230             235                 240
294 Ser Ala Val Gln Asn Leu Val Val Glu Gly Leu Arg Cys Val Val Leu
295              245             250                 255
298 Pro Glu Asp Leu Cys His Lys Phe Leu Gln Leu Ala Glu Ser Asn Thr
299         260             265                 270
302 Val Arg Gly Ile Glu Thr Cys Gly Ile Leu Cys Gly Lys Leu Thr His
303         275             280                 285
306 Asn Glu Phe Thr Ile Thr His Val Ile Val Pro Lys Gln Ser Ala Gly
307     290             295                 300
310 Pro Asp Tyr Cys Asp Met Glu Asn Val Glu Glu Leu Phe Asn Val Gln
311 305             310             315                 320
314 Asp Gln His Asp Leu Leu Thr Leu Gly Trp Ile His Thr His Pro Thr
315              325             330                 335
318 Gln Thr Ala Phe Leu Ser Ser Val Asp Leu His Thr His Cys Ser Tyr
319         340             345                 350
322 Gln Leu Met Leu Pro Glu Ala Ile Ala Ile Val Cys Ser Pro Lys His
323         355             360                 365
326 Lys Asp Thr Gly Ile Phe Arg Leu Thr Asn Ala Gly Met Leu Glu Val
327     370             375                 380
330 Ser Ala Cys Lys Lys Lys Gly Phe His Pro His Thr Lys Glu Pro Arg
331 385             390             395                 400
334 Leu Phe Ser Ile Cys Lys His Val Leu Val Lys Asp Ile Lys Ile Ile
335              405             410                 415
338 Val Leu Asp Leu Arg
339              420
342 <210> SEQ ID NO: 6
343 <211> LENGTH: 461
344 <212> TYPE: PRT
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353 Pro Asp His Thr Asp Val Ser Leu Ser Pro Glu Glu Arg Val Arg Ala
354             20                  25                  30
357 Leu Ser Lys Leu Gly Cys Asn Ile Thr Ile Ser Glu Asp Ile Thr Pro
358             35                  40                  45
361 Arg Arg Tyr Phe Arg Ser Gly Val Glu Met Glu Arg Met Ala Ser Val
362     50                  55                  60
365 Tyr Leu Glu Glu Gly Asn Leu Glu Asn Ala Phe Val Leu Tyr Asn Lys
366 65                  70                  75                  80
369 Phe Ile Thr Leu Phe Val Glu Lys Leu Pro Asn His Arg Asp Tyr Gln
370             85                  90                  95
373 Gln Cys Ala Val Pro Glu Lys Gln Asp Ile Met Lys Lys Leu Lys Glu
374             100                 105                 110
377 Ile Ala Phe Pro Arg Thr Asp Glu Leu Lys Asn Asp Leu Leu Lys Lys
378             115                 120                 125
381 Tyr Asn Val Glu Tyr Gln Glu Tyr Leu Gln Ser Lys Asn Lys Tyr Lys
382     130                 135                 140
385 Ala Glu Ile Leu Lys Lys Leu Glu His Gln Arg Leu Ile Glu Ala Glu
386 145                 150                 155                 160
389 Arg Lys Arg Ile Ala Gln Met Arg Gln Gln Leu Glu Ser Glu Gln
390             165                 170                 175
393 Phe Leu Phe Phe Glu Asp Gln Leu Lys Lys Gln Glu Leu Ala Arg Gly
394             180                 185                 190
397 Gln Met Arg Ser Gln Gln Thr Ser Gly Leu Ser Glu Gln Ile Asp Gly
398     195                 200                 205
401 Ser Ala Leu Ser Cys Phe Ser Thr His Gln Asn Asn Ser Leu Leu Asn
402     210                 215                 220
405 Val Phe Ala Asp Gln Pro Asn Lys Ser Asp Ala Thr Asn Tyr Ala Ser
406 225                 230                 235                 240
409 His Ser Pro Pro Val Asn Arg Ala Leu Thr Pro Ala Ala Thr Leu Ser
410             245                 250                 255
413 Ala Val Gln Asn Leu Val Val Glu Gly Leu Arg Cys Val Val Leu Pro
414             260                 265                 270
417 Glu Asp Leu Cys His Lys Phe Leu Gln Leu Ala Glu Ser Asn Thr Val
418             275                 280                 285
421 Arg Gly Ile Glu Thr Cys Gly Ile Leu Cys Gly Lys Leu Thr His Asn
422     290                 295                 300
425 Glu Phe Thr Ile Thr His Val Ile Val Pro Lys Gln Ser Ala Gly Pro
426 305                 310                 315                 320
429 Asp Tyr Cys Asp Met Glu Asn Val Glu Glu Leu Phe Asn Val Gln Asp
430             325                 330                 335
433 Gln His Asp Leu Leu Thr Leu Gly Trp Ile His Thr His Pro Thr Gln
434             340                 345                 350
437 Thr Ala Phe Leu Ser Ser Val Asp Leu His Thr His Cys Ser Tyr Gln
438             355                 360                 365
441 Leu Met Leu Pro Glu Ala Ile Ala Ile Val Cys Ser Pro Lys His Lys
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 2,4,5,6,7,8,9,10,11,12,13
Seq#:2; Xaa Pos. 3,5,8,9,10,11,12,13,15,16

VERIFICATION SUMMARY   DATE: 06/14/2006
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Input Set : **A:\CIT1510-4.ST25.txt**
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L:47 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:77 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0